SEQUENCE LISTING

<110> Washington State University Research Foundation Mealey, Katrina Bentjen, Steven												
<120> MDR1 VARIANTS AND METHODS FOR THEIR USE												
<130> 4630-61733												
<150> US 60/261,578 <151> 2001-01-12												
<150> US 60/314,829 <151> 2001-08-24												
<160> 10												
<170> PatentIn version 3.1												
<210> 1 <211> 4317 <212> DNA <213> Canis familiaris												
<220> <221> CDS <222> (70)(3912) <223>												
<400> 1 ctaagtegga gtatettett cecaaattee etteteggtg gaggttgega aggaaageee 60												
ctaagtcgga gtatcttctt cccaaattcc cttctcggtg gaggttgcga aggaaagccc 60												
gaggtgacg atg gat cct gaa gga ggc cgt aag ggg agt gca gag aag aac Met Asp Pro Glu Gly Gly Arg Lys Gly Ser Ala Glu Lys Asn 1 5 10												
gaggtgacg atg gat cct gaa gga ggc cgt aag ggg agt gca gag aag aac 111 Met Asp Pro Glu Gly Gly Arg Lys Gly Ser Ala Glu Lys Asn												
gaggtgacg atg gat cct gaa gga ggc cgt aag ggg agt gca gag aag aac Met Asp Pro Glu Gly Gly Arg Lys Gly Ser Ala Glu Lys Asn 1 5 10 ttc tgg aaa atg ggc aaa aaa agt aaa aaa gag aag aaa gaa aag aaa 159 Phe Trp Lys Met Gly Lys Lys Ser Lys Lys Glu Lys Lys												
gaggtgacg atg gat cct gaa gga ggc cgt aag ggg agt gca gag aag aac Met Asp Pro Glu Gly Gly Arg Lys Gly Ser Ala Glu Lys Asn 1 5 10 ttc tgg aaa atg ggc aaa aaa agt aaa aaa gag aag aaa gaa aag aaa Phe Trp Lys Met Gly Lys Lys Ser Lys Lys Glu Lys Lys Glu Lys Lys 15 20 25 30 cca act gtc agc acg ttt gca atg ttt cgc tat tca aat tgg ctt gat Pro Thr Val Ser Thr Phe Ala Met Phe Arg Tyr Ser Asn Trp Leu Asp												
gaggtgacg atg gat cct gaa gga ggc cgt aag ggg agt gca gag aag aac Met Asp Pro Glu Gly Gly Arg Lys Gly Ser Ala Glu Lys Asn 1 5 10 ttc tgg aaa atg ggc aaa aaa agt aaa aaa gag aag aag aaa gaa aag aaa Phe Trp Lys Met Gly Lys Lys Ser Lys Lys Glu Lys Lys Glu Lys Lys 15 20 25 30 cca act gtc agc acg ttt gca atg ttt cgc tat tca aat tgg ctt gat Pro Thr Val Ser Thr Phe Ala Met Phe Arg Tyr Ser Asn Trp Leu Asp 35 40 45 agg ttg tat atg ttg gtg ggg aca atg gct gcc atc atc cat gga gct Arg Leu Tyr Met Leu Val Gly Thr Met Ala Ala Ile Ile His Gly Ala												
gaggtgacg atg gat cct gaa gga ggc cgt aag ggg agt gca gag aag aac act ct gaa gga ggc cgt aag ggg agt gca gag aag aac aal lil Met Asp Pro Glu Gly Gly Arg Lys Gly Ser Ala Glu Lys Asn 1 5 10 ttc tgg aaa atg ggc aaa aaa agt aaa aaa gag aag aag aaa gaa aag aaa Phe Trp Lys Met Gly Lys Lys Ser Lys Lys Glu Lys Lys Glu Lys Lys 15 20 25 30 cca act gtc agc acg ttt gca atg ttt cgc tat tca aat tgg ctt gat Pro Thr Val Ser Thr Phe Ala Met Phe Arg Tyr Ser Asn Trp Leu Asp 35 40 45 agg ttg tat atg ttg gtg ggg aca atg gct gcc atc atc cat gga gct Arg Leu Tyr Met Leu Val Gly Thr Met Ala Ala Ile Ile His Gly Ala 50 55 60 gca ctc cct ctc atg atg ctg gtt ttt gga aac atg aca gat agc ttt Ala Leu Pro Leu Met Met Leu Val Phe Gly Asn Met Thr Asp Ser Phe												

_	atg Met		-		_				-				-		-	4	147
	gtg Val															4	195
_	cag Gln					_						_		_	_	Ē	543
_	gag Glu 160					_	_		_	_		_				Ē	591
	ctc Leu		_	_	-					-				-		6	539
_	gga Gly	_						_									587
	GJA āāā															7	735
_	cct Pro	-					_	_			_	_				7	783
	ttt Phe 240		-				-	_		-		_		_	_	8	331
	gaa Glu															8	379
	aag Lys															Ğ	927
	att Ile															Š	975
	ttc Phe															10)23
	tcc Ser 320															10	071
_	ttc Phe							_		_			-	_		11	L19

									aga Arg 360							1167
									att Ile							1215
									aat Asn							1263
									gtt Val							1311
									gtg Val							1359
	-		-	_	-			_	ctg Leu 440	_	-					1407
									gga Gly							1455
									ggt Gly							1503
									aac Asn						-	1551
									gct Ala							1599
									aaa Lys 520							1647
									cag Gln							1695
									att Ile							1743
_		_	_	_		-	_	-	gca Ala		_	_		_	_	1791
	_	_							att Ile			_		_	_	1839
tct	aca	gtt	cgt	aat	gcc	gat	gtc	att	gct	ggt	ttt	gat	gat	gga	gtc	1887

Ser	Thr	Val	Arg	Asn 595	Ala	Asp	Val	Ile	Ala 600	Gly	Phe	Asp	Asp	Gly 605	Val	
					aat Asn											1935
					aca Thr											1983
					gaa Glu											2031
					660 Gly ggg											2079
					cca Pro											2127
					aat Asn											2175
_	-				gaa Glu						_					2223
					ggc											2271
			-		ttt Phe 740											2319
					ttt Phe					Leu					Ile	2367
					ttc Phe											2415
					cgg Arg											2463
					tgg Trp											2511
					gcc Ala 820											2559
					gtc Val											2607

ggc att att ata tcc tta atc tat ggt tgg caa tta aca ctt tta ctc Gly Ile Ile Ile Ser Leu Ile Tyr Gly Trp Gln Leu Thr Leu Leu Leu tta gca att gta ccc atc att gca ata gca gga gtt gtt gaa atg aaa Leu Ala Ile Val Pro Ile Ile Ala Ile Ala Gly Val Val Glu Met Lys atg ttg tct gga caa gca ctg aaa gat aag aaa gag cta gaa gga gct Met Leu Ser Gly Gln Ala Leu Lys Asp Lys Lys Glu Leu Glu Gly Ala ggg aag att gct aca gaa gcc atc gaa aac ttc cga act gtt gtt tct Gly Lys Ile Ala Thr Glu Ala Ile Glu Asn Phe Arg Thr Val Val Ser ttg act cgg gag cag aag ttt gaa tac atg tat gca cag agt ttg caa Leu Thr Arg Glu Gln Lys Phe Glu Tyr Met Tyr Ala Gln Ser Leu Gln gta cca tac aga aac tct ttg agg aaa gca cac atc ttc ggg gtc tca Val Pro Tyr Arg Asn Ser Leu Arg Lys Ala His Ile Phe Gly Val Ser ttt tct atc acc cag gca atg atg tat ttt tcc tat gct ggc tgt ttc Phe Ser Ile Thr Gln Ala Met Met Tyr Phe Ser Tyr Ala Gly Cys Phe egg ttt ggt gee tae ttg gtg gea aat gag tte atg aac ttt eag gat Arg Phe Gly Ala Tyr Leu Val Ala Asn Glu Phe Met Asn Phe Gln Asp gtt ctt ttg gta ttc tca gct att gtc ttt ggt gcc atg gca gtg ggg Val Leu Leu Val Phe Ser Ala Ile Val Phe Gly Ala Met Ala Val Gly cag gtc agt tca ttt gct cct gac tat gcc aaa gcc aaa gta tca gca Gln Val Ser Ser Phe Ala Pro Asp Tyr Ala Lys Ala Lys Val Ser Ala gcc cac gtc atc atg atc att gaa aaa agc cct ctg att gac agc Ala His Val Ile Met Ile Ile Glu Lys Ser Pro Leu Ile Asp Ser tac agc cct cac ggc ctc aag cca aat acg ttg gaa gga aat gtg Tyr Ser Pro His Gly Leu Lys Pro Asn Thr Leu Glu Gly Asn Val aca ttt aat gag $\,$ gtc gtg ttc aac tat $\,$ ccc act cga cca gac $\,$ atc Thr Phe Asn Glu $\,$ Val Val Phe Asn Tyr $\,$ Pro Thr Arg Pro Asp $\,$ Ile ccc gtg ctc cag $\,$ ggg ctg agc ctc gag $\,$ gtg aag aag ggc cag $\,$ acg $\,$ Pro Val Leu Gln $\,$ Gly Leu Ser Leu Glu $\,$ Val Lys Gly Gln $\,$ Thr ctg gcc ctc gta $\,$ ggt agc agt ggc tgt $\,$ ggg aag agc aca gtt $\,$ gtt Leu Ala Leu Val $\,$ Gly Ser Ser Gly Cys $\,$ Gly Lys Ser Thr Val $\,$ Val $\,$

			gag Glu 1085											cta Leu	3357
	_		aaa Lys 1100					ctg Leu 1105						cga Arg	3402
			ggc Gly 1115												3447
_		-	gag Glu 1130			-			-		_		-	gta Val	3492
			gag Glu 1145					gcc Ala 1150						cac His	3537
			gag Glu 1160					aaa Lys 1165				aga Arg	_	gga Gly	3582
			acc Thr 1175												3627
			gct Ala 1190					cct Pro 1195					ttg Leu 1200	gat Asp	3672
_	_		tca Ser 1205					gaa Glu 1210				gtt Val		caa Gln	3717
_			gac Asp 1220					ggc Gly 1225						atc Ile	3762
			ttg Leu 1235												3807
			ggc Gly 1250												3852
			aaa Lys 1265												3897
	gca Ala		_	tag	tgaa	actg	agg (ccata	tgag	c tgi	taaa	atat	tttt	taatat	3952
ttg [.]	tgtta	aaa a	acatg	gcati	taa	atcaa	aagt	taaaa	aggto	ga go	cacti	tacto	g gaaa	aaactat	4012
gta	gaact	tac o	ctgtt	taaca	a tti	tctt	gctg	caac	tgaa	ga to	catt	ccac	c aag	ttcagag	4072

tcttcagatt ttataattaa aggaaccaaa agaaacatta tctgatggaa taaaatattg	4132
gtgttaattg cattataaaa ttatagagta attcaaagta gattttgtta ataaattgta	4192
taatttttgt ttatatttta tttgtaactt actgctttgc tgaaagatta tagaagtggt	4252
aaaaagtact gaatgtttga ataaagtgct agctataata aaactaaact	4312
aaaaa	4317
<210> 2 <211> 1280 <212> PRT <213> Canis familiaris	

<400> 2

Met Asp Pro Glu Gly Gly Arg Lys Gly Ser Ala Glu Lys Asn Phe Trp $1 \hspace{1.5cm} 5 \hspace{1.5cm} 10 \hspace{1.5cm} 15$

Lys Met Gly Lys Lys Ser Lys Lys Glu Lys Lys Glu Lys Lys Pro Thr 20 25 30

Val Ser Thr Phe Ala Met Phe Arg Tyr Ser Asn Trp Leu Asp Arg Leu 35 40 45

Tyr Met Leu Val Gly Thr Met Ala Ala Ile Ile His Gly Ala Ala Leu $50 \hspace{1cm} 55 \hspace{1cm} 60$

Pro Leu Met Met Leu Val Phe Gly Asn Met Thr Asp Ser Phe Ala Asn 65 70 75 80

Ala Gly Ile Ser Arg Asn Lys Thr Phe Pro Val Ile Ile Asn Glu Ser 85 90 95

Ile Thr Asn Asn Thr Gln His Phe Ile Asn His Leu Glu Glu Glu Met 100 105 110

Thr Thr Tyr Ala Tyr Tyr Tyr Ser Gly Ile Gly Ala Gly Val Leu Val 115 120 125

Ala Ala Tyr Ile Gln Val Ser Phe Trp Cys Leu Ala Ala Gly Arg Gln 130 135 140

Ile Leu Lys Ile Arg Lys Gln Phe Phe His Ala Ile Met Arg Gln Glu 145 150 155 160

Ile Gly Trp Phe Asp Val His Asp Val Gly Glu Leu Asn Thr Arg Leu 165 170 175

Thr Asp Asp Val Ser Lys Ile Asn Glu Gly Ile Gly Asp Lys Val Gly 180 185 190

Met Phe Phe Gln Ser Ile Ala Thr Phe Phe Thr Gly Phe Ile Val Gly 195 200 205

Phe Thr Pro Gly Trp Lys Leu Thr Leu Val Ile Leu Ala Ile Ser Pro 210 215 220

Val Leu Gly Leu Ser Ala Ala Ile Trp Ala Lys Ile Leu Ser Ser Phe 225 230 235 240

Thr Asp Lys Glu Leu Leu Ala Tyr Ala Lys Ala Gly Ala Val Ala Glu 245 250 255

Glu Val Leu Ala Ala Ile Arg Thr Val Ile Ala Phe Gly Gly Gln Lys $260 \hspace{1.5cm} 265 \hspace{1.5cm} 270 \hspace{1.5cm}$

Lys Glu Leu Glu Arg Tyr Asn Lys Asn Leu Glu Glu Ala Lys Arg Ile 275 280 285

Gly Ile Lys Lys Ala Ile Thr Ala Asn Ile Ser Ile Gly Ala Ala Phe 290 295 300

Leu Leu Ile Tyr Ala Ser Tyr Ala Leu Ala Phe Trp Tyr Gly Thr Ser 305 310 315 320

Leu Val Leu Ser Ser Glu Tyr Thr Ile Gly Gln Val Leu Thr Val Phe 325 330 335

Phe Ser Val Leu Ile Gly Ala Phe Ser Ile Gly Gln Ala Ser Pro Ser 340 345 350

Ile Glu Ala Phe Ala Asn Ala Arg Gly Ala Ala Tyr Glu Ile Phe Lys 355 360 365

Ile Ile Asp Asn Lys Pro Ser Ile Asp Ser Tyr Ser Lys Ser Gly His 370 380

Lys Pro Asp Asn Ile Lys Gly Asn Leu Glu Phe Lys Asn Val His Phe 385 390 395 400

Ser Tyr Pro Ser Arg Lys Glu Val Lys Ile Leu Lys Gly Leu Asn Leu 405 410 415

Lys Val Gln Ser Gly Gln Thr Val Ala Leu Val Gly As
n Ser Gly Cys 420 425 430

Gly Lys Ser Thr Thr Val Gln Leu Met Gln Arg Leu Tyr Asp Pro Thr 435 440 445

Asp Gly Met Val Cys Ile Asp Gly Gln Asp Ile Arg Thr Ile Asn Val 450 455 460

Arg His Leu Arg Glu Ile Thr Gly Val Val Ser Gln Glu Pro Val Leu 465 470 475 480

Thr Met Asp Glu Ile Glu Lys Ala Val Lys Glu Ala Asn Ala Tyr Asp 500 505 510

Phe Ile Met Lys Leu Pro Asn Lys Phe Asp Thr Leu Val Gly Glu Arg 515 520 525

Gly Ala Arg Leu Ser Gly Gly Gln Lys Gln Arg Ile Ala Ile Ala Arg 530 540

Ala Leu Val Arg Asn Pro Lys Ile Leu Leu Leu Asp Glu Ala Thr Ser 545 550 555 560

Ala Leu Asp Thr Glu Ser Glu Ala Val Val Gln Val Ala Leu Asp Lys 565 570 575

Ala Arg Lys Gly Arg Thr Thr Ile Val Ile Ala His Arg Leu Ser Thr 580 585 590

Val Arg Asn Ala Asp Val Ile Ala Gly Phe Asp Asp Gly Val Ile Val 595 600 605

Glu Lys Gly Asn His Asp Glu Leu Met Lys Glu Lys Gly Ile Tyr Phe 610 615 620

Lys Leu Val Thr Met Gln Thr Arg Gly Asn Glu Île Glu Leu Glu Asn 625 630 635 640

Ala Thr Gly Glu Ser Lys Ser Glu Ser Asp Ala Leu Glu Met Ser Pro 645 650 655

Lys Asp Ser Gly Ser Ser Leu Ile Lys Arg Arg Ser Thr Arg Arg Ser

660 665 670

Ile	His	Ala 675	Pro	Gln	Gly	Gln	Asp 680	Arg	Lys	Leu	Gly	Thr 685	Lys	Glu	Asp
Leu	Asn 690	Glu	Asn	Val	Pro	Ser 695	Val	Ser	Phe	Trp	Arg 700	Ile	Leu	Lys	Leu
Asn 705	Ser	Thr	Glu	Trp	Pro 710	Tyr	Phe	Val	Val	Gly 715	Ile	Phe	Cys	Ala	Ile 720
Ile	Asn	Gly	Gly	Leu 725	Gln	Pro	Ala	Phe	Ser 730	Ile	Ile	Phe	Ser	Arg 735	Ile
Ile	Gly	Ile	Phe 740	Thr	Arg	Asp	Glu	Asp 745	Pro	Glu	Thr	Lys	Arg 750	Gln	Asn
Ser	Asn	Met 755	Phe	Ser	Val	Leu	Phe 760	Leu	Val	Leu	Gly	Ile 765	Ile	Ser	Phe
Ile	Thr 770	Phe	Phe	Leu	Gln	Gly 775	Phe	Thr	Phe	Gly	Lys 780	Ala	Gly	Glu	Ile
Leu 785	Thr	Lys	Arg	Leu	Arg 790	Tyr	Met	Val	Phe	Arg 795	Ser	Met	Leu	Arg	Gln 800
Asp	Val	Ser	Trp	Phe 805	Asp	Asp	Pro	Lys	Asn 810	Thr	Thr	Gly	Ala	Leu 815	Thr
Thr	Arg	Leu	Ala 820	Asn	Asp	Ala	Ala	Gln 825	Val	Lys	Gly	Ala	Ile 830	Gly	Ser
Arg	Leu	Ala 835	Val	Ile	Thr	Gln	Asn 840	Ile	Ala	Asn	Leu	Gly 845	Thr	Gly	Ile
Ile	Ile 850	Ser	Leu	Ile	Tyr	Gly 855	Trp	Gln	Leu	Thr	Leu 860	Leu	Leu	Leu	Ala
Ile 865	Val	Pro	Ile	Ile	Ala 870	Ile	Ala	Gly	Val	Val 875	Glu	Met	Lys	Met	Leu 880
Ser	Gly	Gln	Ala	Leu 885	Lys	Asp	Lys	Lys	Glu 890	Leu	Glu	Gly	Ala	Gly 895	Lys
Ile	Ala	Thr	Glu 900	Ala	Ile	Glu	Asn	Phe 905	Arg	Thr	Val	Val	Ser 910	Leu	Thr

Arg Glu Gln Lys Phe Glu Tyr Met Tyr Ala Gln Ser Leu Gln Val Pro 915 920 925

Tyr Arg Asn Ser Leu Arg Lys Ala His Ile Phe Gly Val Ser Phe Ser 930 935 940

Ile Thr Gln Ala Met Met Tyr Phe Ser Tyr Ala Gly Cys Phe Arg Phe945950955960

Gly Ala Tyr Leu Val Ala Asn Glu Phe Met Asn Phe Gln Asp Val Leu 965 970 975

Leu Val Phe Ser Ala Ile Val Phe Gly Ala Met Ala Val Gly Gln Val 980 985 990

Ser Ser Phe Ala Pro Asp Tyr Ala Lys Ala Lys Val Ser Ala Ala His 995 1000 1005

Val Ile Met Ile Ile Glu Lys Ser Pro Leu Ile Asp Ser Tyr Ser 1010 1015 1020

Pro His Gly Leu Lys Pro Asn Thr Leu Glu Gly Asn Val Thr Phe 1025 1030 1035

Asn Glu Val Val Phe Asn Tyr Pro Thr Arg Pro Asp Ile Pro Val 1040 1045 1050

Leu Gln Gly Leu Ser Leu Glu Val Lys Lys Gly Gln Thr Leu Ala 1055 1060 1065

Leu Val Gly Ser Ser Gly Cys Gly Lys Ser Thr Val Val Gln Leu 1070 1075 1080

Leu Glu Arg Phe Tyr Asp Pro Leu Ala Gly Ser Val Leu Ile Asp 1085 1090 1095

Gly Lys Glu Ile Lys His Leu Asn Val Gln Trp Leu Arg Ala His 1100 1105 1110

Leu Gly Ile Val Ser Gln Glu Pro Ile Leu Phe Asp Cys Ser Ile 1115 1120 1125

Ala Glu Asn Ile Ala Tyr Gly Asp Asn Ser Arg Val Val Ser His 1130 1135 1140

Glu	Glu 1145		Met	Gln	Ala	Ala 1150	Lys	Glu	Ala	Asn	Ile 1155	His	His	Phe	
Ile	Glu 1160		Leu	Pro	Glu	Lys 1165	Tyr	Asn	Thr	Arg	Val 1170	Gly	Asp	Lys	
Gly	Thr 1175		Leu	Ser	Gly	Gly 1180	Gln	Lys	Gln	Arg	Ile 1185	Ala	Ile	Ala	
Arg	Ala 1190		Val	Arg	Gln	Pro 1195	His	Ile	Leu	Leu	Leu 1200	Asp	Glu	Ala	
Thr	Ser 1205		Leu	Asp	Thr	Glu 1210	Ser	Glu	Lys	Val	Val 1215	Gln	Glu	Ala	
Leu	Asp 1220		Ala	Arg	Glu	Gly 1225	Arg	Thr	Cys	Ile	Val 1230	Ile	Ala	His	
Arg	Leu 1235		Thr	Ile	Gln	Asn 1240	Ala	Asp	Leu	Ile	Val 1245	Val	Phe	Gln	
Asn	Gly 1250		Val	Lys	Glu	His 1255	Gly	Thr	His	Gln	Gln 1260	Leu	Leu	Ala	
Gln	Lys 1265		Ile	Tyr	Phe	Ser 1270	Met	Ile	Ser	Val	Gln 1275	Ala	Gly	Ala	
Lys	Arg 1280														
<210 <211 <212 <213	?> D	0 NA	etic	olig	gonu	cleot	ide								
<400 tccg)> 3 ıgttt		gccta	actto	3										20
<210 <211 <212 <213	> 2 ?> D	1 NA	etic	olig	gonu	cleot:	ide								
<400 tgct	> 4	ga c	tttg	ccatt	С										21
<210 <211															

<212> <213>	DNA synthetic oligonucleotide	
<400> cctcac	5 taag cggcttcgat ac	22
<210>	6	
<211>	22	
<212>		
<213>	synthetic oligonucleotide	
<400>	6	
aaacag	gatg ggctcctgag ac	22
<210>	7	
<211>		
<212> <213>		
(213)	Synthetic Oligonacieotiae	
<400>	7	
cagcac	gttt gcaatgtttc	20
<210>		
<211>		
<212> <213>		
	Dynametre offgonderectide	
<400>	8	
tctggt	ttat gtccactctt cg	22
<210>		
<211>		
<212> <213>	DNA synthetic oligonucleotide	
(210)	Synthetic Oligonaciottae	
<400>	9	0.1
aggcat	cccc aagcattgaa g	21
<210>	10	
<211> <212>	20 DNA	
<213>	synthetic oligonucleotide	
<400>	10	20
tgagcc	gcat cattggcaag	20